PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:47

INPUT SET: S36517.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING	ENTERS
2 3	(1)	General Information	5 2 2
4 5 6		(i) APPLICANT: Hillman, Jennifer L. Goli, Surya K.	# 2
7 8 9		(ii) TITLE OF THE INVENTION: NOVEL CALCIUM-BINDIN PROTEIN	ig .
10 11 12		(iii) NUMBER OF SEQUENCES: 4	
13 14 15 16 17 18		<pre>(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Incyte Pharmaceuticals, Inc. (B) STREET: 3174 Porter Drive (C) CITY: Palo Alto (D) STATE: CA (E) COUNTRY: USA (F) ZIP: 94304</pre>	
20 21 22 23 24 25	·	(v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Diskette (B) COMPUTER: IBM Compatible (C) OPERATING SYSTEM: DOS (D) SOFTWARE: FastSEQ for Windows Version 2.0	
26 27 28 29 30		(vi) CURRENT APPLICATION DATA:(A) APPLICATION NUMBER: 09/768,840(B) FILING DATE:(C) CLASSIFICATION:	
31 32 33 34 35		<pre>(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 09/206,499 (B) FILING DATE:</pre>	•
36 37 38 39 40		(viii) ATTORNEY/AGENT INFORMATION:(A) NAME: Billings, Lucy J.(B) REGISTRATION NUMBER: 36,749(C) REFERENCE/DOCKET NUMBER: PF-0261 US	
41 42 43 44 45		(ix) TELECOMMUNICATION INFORMATION:(A) TELEPHONE: 415-855-0555(B) TELEFAX: 415-845-4166	
46		(2) INFORMATION FOR SEQ ID NO:1:	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:47

INPUT SET: S36517.raw

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47
            (i) SEQUENCE CHARACTERISTICS:
48
              (A) LENGTH: 328 amino acids
49
              (B) TYPE: amino acid
50
              (C) STRANDEDNESS: single
51
              (D) TOPOLOGY: linear
52
53
            (vii) IMMEDIATE SOURCE:
54
               (A) LIBRARY: CONUTUT01
55
               (B) CLONE: 2509570
56
57
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59
      Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His
60
61
      Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
62
63
                  20
                                      25
      Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
64
65
                                  40
      His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
66
67
                              55
      Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
68
69
                          70
70
      Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
71
      Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
72
73
                                      105
      His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
74
75
                                  120
                                                       125
      Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
76
77
                              135
78
     His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
79
                          150
                                              155
      Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
80
81
                                          170
     Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
82
83
                                     185
     His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
84
85
                                  200
86
     Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
87
                             215
     Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
88
89
                                              235
                         230
     Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
90
91
                     245 .
                                          250
     Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
92
93
                 260
                                      265
     Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
94
95
                                  280
     Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
96
97
                             295
     Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
98
99
                          310
                                              315
```

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:47

INPUT SET: S36517.raw

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Leu Thr Arg His His Asp Glu Leu
100
                       325
101
102
                (2) INFORMATION FOR SEQ ID NO:2:
103
104
            (i) SEQUENCE CHARACTERISTICS:
105
               (A) LENGTH: 1055 base pairs
106
               (B) TYPE: nucleic acid
107
               (C) STRANDEDNESS: single
108
               (D) TOPOLOGY: linear
109
110
             (vii) IMMEDIATE SOURCE:
111
                (A) LIBRARY: CONTUT01
112
                (B) CLONE: 2509570
113
114
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116
       GGAGAGCGGA NGNANTGGNA TAACAGGGGA CCGATGATGT GGCGACCATC AGTTCTGCTG
                                                                               60
117
       CTTCTGTTGC TACTGAGGCA CGGGGCCCAG GGGAAGCCAT CCCCAGACGC AGGCCCTCAT
                                                                              120
118
      GGCCAGGGGA GGGTGCACCA GGCGGCCCCC CTGAGCGACG CTCCCCATGA TGACGCCCAC
                                                                              180
119
       GGGAACTTCC AGTACGACCA TGAGGCTTTC CTGGGACGGG AAGTGGCCAA GGAATTCGAC
                                                                              240
120
       CAACTCACCC CAGAGGAAAG CCAGGCCCGT CTGGGGCGGA TCGTGGACCG CATGGACCGC
                                                                              300
121
       GCGGGGGACG GCGACGCTG GGTGTCGCTG GCCGAGCTTC GCGCGTGGAT CGCGCACACG
                                                                              360
122
       CAGCAGCGGC ACATACGGGA CTCGGTGAGC GCGGCCTGGG ACACGTACGA CACGGACCGC
                                                                             . 420
123
       GACGGGCGTG TGGGTTGGGA GGAGCTGCGC AACGCCACCT ATGGCCACTA CGCGCCCGGT
                                                                              480
124
      GAAGAATTTC ATGACGTGGA GGATGCAGAG ACCTACAAAA AGATGCTGGC TCGGGACGAG
                                                                              540
125
       CGGCGTTTCC GGGTGGCCGA CCAGGATGGG GACTCGATGG CCACTCGAGA GGAGCTGACA
                                                                              600
126
       GCCTTCCTGC ACCCCGAGGA GTTCCCTCAC ATGCGGGACA TCGTGATTGC TGAAACCCTG
                                                                              660
127
       GAGGACCTGG ACAGAAACAA AGATGGCTAT GTCCAGGTGG AGGAGTACAT CGCGGATCTG
                                                                              720
128
       TACTCAGCCG AGCCTGGGGA GGAGGAGCCG GCGTGGGTGC AGACGGAGAG GCAGCAGTTC
                                                                              780
129
       CGGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG GGAGTGAGGT GGGCCACTGG
                                                                              840
130
       GTGCTGCCCC CTGCCCAGGA CCAGCCCCTG GTGGAAGCCA ACCACCTGCT GCACGAGAGC
                                                                              900
131
       GACACGGACA AGGATGGGCG GCTGAGCAAA GCGGAAATCC TGGGTAATTG GAACATGTTT
                                                                              960
132
       GTGGGCAGTC AGGCCACCAA CTATGGCGAG GACCTGACCC GGCACCACGA TGAGCTGTGA
                                                                             1020
133
                                                                             1055
       GCACCGCGCA CCTGCCACAG CCTCAGAGGC CCGCA
134
135
                (2) INFORMATION FOR SEQ ID NO:3:
136
137
             (i) SEQUENCE CHARACTERISTICS:
138
               (A) LENGTH: 331 amino acids
139
               (B) TYPE: amino acid
140
               (C) STRANDEDNESS: single
141
               (D) TOPOLOGY: linear
142
143
             (vii) IMMEDIATE SOURCE:
144
                 (A) LIBRARY: GenBank
145
                 (B) CLONE: 1262329
146
147
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
148
149
       Met Ala Arg Gly Gly Arg Gly Arg Leu Gly Leu Ala Leu Gly Leu
150
                                            10
                         5
151
       Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
```

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:48

INPUT SET: S36517.raw

```
25
153
      Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
154
                                  40
155
      Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
156
157
      Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
158
                          70
                                              75
159
      Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
160
                                          90
161
                     85
      Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
162
                                      105
163
                  100
      Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
164
                   120
165
      Arg Asp Lys Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
166
                                                  140
                             135
167
      Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
168
                                             155
                          150
169
      His His Thr Phe Lys Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
170
                                         170
                      165
171
      Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
172
                                                        190
       180
                                      185
173
      Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
174
                                  200
              195
175
      Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
176
                              215
177
      Gln Asp Glu Tyr Ile Ala Asp Met Phe Ser His Glu Glu Asn Gly Pro
178
                                              235
                          230
179
      Glu Pro Asp Trp Val Leu Ser Glu Arg Glu Gln Phe Asn Glu Phe Arg
180
                                          250
                      245
181
      Asp Leu Asn Lys Asp Gly Lys Leu Asp Lys Asp Glu Ile Arg His Trp
182
                                      265
183
      Ile Leu Pro Gln Asp Tyr Asp His Ala Gln Ala Glu Ala Arg His Leu
184
                                  280
185
      Val Tyr Glu Ser Asp Lys Asn Lys Asp Glu Lys Leu Thr Lys Glu Glu
186
                              295
                                                  300
187
      Ile Leu Glu Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr
188
                                                                  320
                                              315
189
                          310
      Gly Glu Asp Leu Thr Lys Asn His Asp Glu Leu
190
                      325
191
192
                (2) INFORMATION FOR SEQ ID NO:4:
193
194
             (i) SEQUENCE CHARACTERISTICS:
195
               (A) LENGTH: 325 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS: single
198
               (D) TOPOLOGY: linear
199
200
             (vii) IMMEDIATE SOURCE:
201
                (A) LIBRARY: GenBank
202
                (B) CLONE: 220582
203
204
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:48

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206	Met 2	7 l a	A ra	Glv I	Glv.	Arq	Leu	Gly	Leu	Ala	Leu	Gly	Leu	Leu	Leu	Ala
.207	met .	Ald	Arg	Gry	5	J		_		10				~1	15	wal.
208	1 Leu	va 1	T.en	Ala	Leu	Arg	Ala	Lys	Pro	Thr	Val	Arg	Lys	GIU	Arg	Vai
209	пеп	vaı	ПСМ	20		•			25			_	a1	30	A cn	Gln.
210	Val	Δra	Pro	Asp	Ser	Glu	Leu	Gly	Glu	Arg	Pro	Pro	GIU	ASP	WPII	GIII
211 212	Vai	9	35					40				-	45	A cro	Car	LVS
212	Ser	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	СтХ	гуs	GIU	Asp	JCI	272
213	501	50		•			55			_	-	60	720	T.011	Glv	Lvs
215	Thr	Phe	Asp	Gln	Leu	Ser	Pro	Asp	Glu	Ser	гуs	GIU	Arg	БСи	0-1	80
216	65		-			70				•	75	T 011	t/a l	Thr	Thr	Glu
217	Ile	Val	Asp	Arg	Ile	Asp	ser	Asp	GТĀ	Asp	GIY	пец	Val		95	_
218					85				1	90	Tire	λνα	Tvr	Tle	Tvr	Asp
219	Glu	Leu	Lys	Leu	Trp	Ile	Lys	Arg	vai	GIII	пур	LT. A	-1-	110	•	_
220				100	_			3	105	Λen	Δrσ	Asp	Lvs	Asp	Glu	Lys
221	Asn	Val	Ala	Lys	Val	Trp	Lys	Asp	IÀT	АЗР	nr 9		125	•		Lys
222			115			_	.	120	λla	Thr	Tvr	Glv	Tyr	Tyr	Leu	Gly
223	Ile	Ser	Trp	Glu	Glu	Tyr	ьуs 135	GIII	ATG	1114	-1-	140	•			•
224		130			_1	***	732	Car	Ser	Asp	His	His	Thr	Phe	Lys	Lys 160
225	Asn	Pro	Ala	Glu	Pne	150	Asp	261	501		155					160
226	145		_		7 ~~	150	Δra	Δτα	Phe	Lys	Ala	Ser	Asp	Leu	Asp	Gly
227	Met	Lev	Pro	Arg	ASP	GIU	nr 9	9		170)				175	· -
228		_	m1		TOD	Ara	Glu	Glu	Phe	Thr	Ala	Phe	Lev	His	Pro	Glu
229	Asp	Let	Tnr	100	TIIT	AT 9	010		185	,				190)	
230	3	Dh.		TOU Tie	Met	Lvs	Glu	ı Ile	val	val	Lev	Glu	Thr	Lev	ı GI	ı Asp
231	GIU	Pne	105	:	rico			200)				205	5		
232	T 10	7 01	1379	, ΣΔsn	Glv	Ast	Gly	/ Phe	val	Asp	o Glr	ı Ası	Gli	і Туі	C TT6	e Ala
233	116	210	יע ה	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	. 0-7		215	5			_	220)		~ T/~	l Leu
234 235	λen	Met	- Phe	e Ser	His	Glu	ı Ası	Asr	ı Gly	Pro	o Gli	ı Pro	o Asp	o Tri	ya.	1 Leu 240
235	225					230)				239	5 • • • •	. 10	n T 17	e 7\e1	n Glv
237	Ser	Gl	u Arc	g Glu	ı Glr	ı Phe	e Ası	n Ası	Phe	e Arg	g Asj	о те	J AS	n ny.	25	p Gly 5
238	501				245	5				25	0 7.	- TO	, Dr	പ	n As	n Tvr
239	Lvs	Le	u Asj	р Буя	s Asy	Glı	ı Ile	e Arg	y His	s Tr	р тт	e ne	u Fr	27	0	p Tyr
240	-2			260)		_	_	26	5 T 0	. 175	ገ ጥኒ/	r Gl	u Se	r As	p Lys
241	Asy	Hi	s Al	a Glı	n Ala	a Glu	u Ala	a Ar	д нт	s he	u va		28	5		p Lys
242	_		27	5			1	28	U a (1)	u <u>(1</u> 1	,, T1	e Tie	u As	p As	n Tr	p Asn
243	Ası	а Ьу	s As	p Gl	u Met	t Le	u Th	- г. г.	S G1	u GI	u 11	30	0	•		p Asn
244		29	0		_	~ 7	29	ე ე ლ Խ	~ Ac	n ጥህ	r Gl	v Gl	u As	p Le	u Th	r Lys 320
245	Me	t Ph	e Va	l Gl	y Se	r GI	u at	a III	T WO	Y	31	, 5		-		320
246	30!	5				31	U									
247	Ası	n Hi	s As	p Gl	u ье	u E										
248					32	J										
249																

PAGE: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/768,840

DATE: 03/15/2001 TIME: 22:39:48

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Original Text